

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/599,974C

1646

DATE: 07/29/98
TIME: 10:06:50

INPUT SET: S27758.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Friedman, Jeffrey M.
Lee, Gwo-Hua
Proenca, Ricardo

(ii) TITLE OF INVENTION: DB, THE RECEPTOR FOR LEPTIN, NUCLEIC
ACIDS ENCODING THE RECEPTOR, AND USES THEREOF

(iii) NUMBER OF SEQUENCES: 56

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: David A. Jackson, Esq.
(B) STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
(C) CITY: Hackensack
(D) STATE: New Jersey
(E) COUNTRY: USA
(F) ZIP: 07601

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/599,974
(B) FILING DATE: 14-FEB-1996
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/586,594
(B) FILING DATE: 16-JAN-1996
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Jackson Esq., David A.
(B) REGISTRATION NUMBER: 26,742
(C) REFERENCE/DOCKET NUMBER: 600-1-162 CP1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 201-487-5800
(B) TELEFAX: 201-343-1684

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/599,974CDATE: 07/29/98
TIME: 10:06:51

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2529 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: A15 (OB-Ra)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGGCTCAGGT	CGGCGTCGTA	CCAGCCGCTG	AAGCGGTTCT	CCAGGTTCCA	GGCGCTCTCG	60
CCATGCCCGGA	TCAGCACCAG	CTTGTTAGCTC	GTGCCGAATT	CGGCACGAGG	TTGCTTTGGG	120
AATGAGCAAG	GTCAAAACTG	CTCTGCACTC	ACAGACAACA	CTGAAGGGAA	GACACTGGCT	180
TCAGTAGTGA	AGGCTTCAGT	TTTTCGCCAG	CTAGGTGTAA	ACTGGGACAT	AGAGTGCTGG	240
ATGAAAGGGG	ACTTGACATT	ATTCATCTGT	CATATGGAGC	CATTACCTAA	GAACCCCTTC	300
AAGAATTATG	ACTCTAAGGT	CCATCTTTTA	TATGATCTGC	CTGAAGTCAT	AGATGATTCG	360
CCTCTGCCCC	CACTGAAAGA	CAGCTTTTCAG	ACTGTCCAAT	GCAACTGCAG	TCTTCGGGGA	420
TGTGAATGTC	ATGTGCCGGT	ACCCAGAGCC	AAACTCAACT	ACGCTCTTCT	GATGTATTTG	480
GAAATCACAT	CTGCCGGTGT	GAGTTTTTCAG	TCACCTCTGA	TGTCACTGCA	GCCCATGCTT	540
GTTGTGAAAC	CCGATCCACC	CTTAGGTTTG	CATATGGAAG	TCACAGATGA	TGGTAATTTA	600
AAGATTTCTT	GGGACAGCCA	AACAATGGCA	CCATTTCCGC	TTCAATATCA	GGTGAAATAT	660
TTAGAGAATT	CTACAATTGT	AAGAGAGGCT	GCTGAAATTG	TCTCAGCTAC	ATCTCTGCTG	720
GTAGACAGTG	TGCTTCCTGG	ATCTTCATAT	GAGGTCCAGG	TGAGGAGCAA	GAGACTGGAT	780
GGTTCAGGAG	TCTGGAGTGA	CTGGAGTTCA	CCTCAAGTCT	TTACCACACA	AGATGTTGTG	840
TATTTTCCAC	CCAAAATTCT	GACTAGTGTT	GGATCGAATG	CTTCTTTTCA	TTGCATCTAC	900

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100								
101	AAAAACGAAA	ACCAGATTAT	CTCCTCAAAA	CAGATAGTTT	GGTGGAGGAA	TCTAGCTGAG		960
102								
103	AAAAATCCCTG	AGATACAGTA	CAGCATTGTG	AGTGACCGAG	TTAGCAAAGT	TACCTTCTCC		1020
104								
105	AACCTGAAAG	CCACCAGACC	TCGAGGGAAG	TTTACCTATG	ACGCAGTGTA	CTGCTGCAAT		1080
106								
107	GAGCAGGCGT	GCCATCACCG	CTATGCTGAA	TTATACGTGA	TCGATGTCAA	TATCAATATA		1140
108								
109	TCATGTGAAA	CTGACGGGTA	CTTAACATAA	ATGACTTGCA	GATGGTCACC	CAGCACAATC		1200
110								
111	CAATCACTAG	TGGGAAGCAC	TGTGCAGCTG	AGGTATCACA	GGCGCAGCCT	GTATTGTCCCT		1260
112								
113	GATAGTCCAT	CTATTTCATC	TACGTCTGAG	CCCCAAAACT	GCGTCTTACA	GAGAGACGGC		1320
114								
115	TTTTATGAAT	GTGTTTTCCA	GCCAATCTTT	CTATTATCTG	GCTATACAAT	GTGGATCAGG		1380
116								
117	ATCAACCATT	CTTTAGGTTC	ACTTGACTCG	CCACCAACGT	GTGTCCCTTC	TGACTCCGTA		1440
118								
119	GTAAAACAC	TACCTCCATC	TAACGTAAAA	GCAGAGATTA	CTGTAAACAC	TGGATTATTG		1500
120								
121	AAAGTATCTT	GGGAAAAGCC	AGTCTTTCCG	GAGAATAACC	TTCAATTCCA	GATTTCGATAT		1560
122								
123	GGCTTAAGTG	GAAAAAGAAAT	ACAATGGAAG	ACACATGAGG	TATTCGATGC	AAAGTCAAAG		1620
124								
125	TCTGCCAGCC	TGCTGGTGTC	AGACCTCTGT	GCAGTCTATG	TGGTCCAGGT	TCGCTGCCGG		1680
126								
127	CGGTTGGATG	GACTAGGATA	TTGGAGTAAT	TGGAGCAGTC	CAGCCTATAC	GCTTGTCTATG		1740
128								
129	GATGTAAAAG	TTCTTATGAG	AGGGCCTGAA	TTTTGGAGAA	AAATGGATGG	GGACGTTACT		1800
130								
131	AAAAAGGAGA	GAAATGTCAC	CTTGCTTTGG	AAGCCCCCTGA	CGAAAAATGA	CTCACTGTGT		1860
132								
133	AGTGTGAGGA	GGTACGTGGT	GAAGCATCGT	ACTGCCCACA	ATGGGACGTG	GTCAGAAGAT		1920
134								
135	GTGGGAAATC	GGACCAATCT	CACTTTCCCTG	TGGACAGAAC	CAGCGCACAC	TGTTACAGTT		1980
136								
137	CTGGCTGTCA	ATTCCCTCGG	CGCTTCCCTT	GTGAATTTTA	ACCTTACCTT	CTCATGGCCC		2040
138								
139	ATGAGTAAAG	TGAGTGCTGT	GGAGTCACTC	AGTGCTTATC	CCCTGAGCAG	CAGCTGTGTC		2100
140								
141	ATCCTTTTCT	GGACACTGTC	ACCTGATGAT	TATAGTCTGT	TATATCTGGT	TATTGAATGG		2160
142								
143	AAGATCCTTA	ATGAAGATGA	TGGAATGAAG	TGGCTTAGAA	TTCCCTCGAA	TGTTAAAAAG		2220
144								
145	TTTTATATCC	ACGATAATTT	TATTCCCATC	GAGAAATATC	AGTTTAGTCT	TTACCCAGTA		2280
146								
147	TTTATGGAAG	GAGTTGGAAG	ACCAAAGATA	ATTAATGGTT	TCACCAAAGA	TGCTATCGAC		2340
148								
149	AAGCAGCAGA	ATGACGCAGG	GCTGTATGTC	ATTGTACCCA	TAATTATTTT	CTCTTGTGTC		2400
150								
151	CTACTGCTCG	GAACACTGTT	AATTTACAC	CAGAGAAATGA	AAAAGTTGTT	TTGGGACGAT		2460
152								

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153 GTTCCAAACC CCAAGAATTG TTCCTGGGCA CAAGGACTGA ATTTCCAAAA GAGAACGGAC 2520

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155 ACTCTTTGA

2529

156

157 (2) INFORMATION FOR SEQ ID NO:2:

158

159 (i) SEQUENCE CHARACTERISTICS:

160 (A) LENGTH: 842 amino acids

161 (B) TYPE: amino acid

162 (C) STRANDEDNESS: Not Relevant

163 (D) TOPOLOGY: Not Relevant

164

165 (ii) MOLECULE TYPE: protein

166

167 (iii) HYPOTHETICAL: NO

168

169 (iv) ANTI-SENSE: NO

170

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172 (vii) IMMEDIATE SOURCE:

173 (B) CLONE: OB-Ra

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177 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

178

179 Gly Leu Arg Ser Ala Ser Tyr Gln Pro Leu Lys Arg Phe Ser Arg Phe
180 1 5 10 15

181

182 Gln Ala Leu Ser Pro Cys Arg Ile Ser Thr Ser Leu Xaa Leu Val Pro
183 20 25 30

184

185 Asn Ser Ala Arg Gly Cys Phe Gly Asn Glu Gln Gly Gln Asn Cys Ser
186 35 40 45

187

188 Ala Leu Thr Asp Asn Thr Glu Gly Lys Thr Leu Ala Ser Val Val Lys
189 50 55 60

190

191 Ala Ser Val Phe Arg Gln Leu Gly Val Asn Trp Asp Ile Glu Cys Trp
192 65 70 75 80

193

194 Met Lys Gly Asp Leu Thr Leu Phe Ile Cys His Met Glu Pro Leu Pro
195 85 90 95

196

197 Lys Asn Pro Phe Lys Asn Tyr Asp Ser Lys Val His Leu Leu Tyr Asp
198 100 105 110

199

200 Leu Pro Glu Val Ile Asp Asp Ser Pro Leu Pro Pro Leu Lys Asp Ser
201 115 120 125

202

203 Phe Gln Thr Val Gln Cys Asn Cys Ser Leu Arg Gly Cys Glu Cys His
204 130 135 140

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206	Val	Pro	Val	Pro	Arg	Ala	Lys	Leu	Asn	Tyr	Ala	Leu	Leu	Met	Tyr	Leu
207	145					150					155					160
208																
209	Glu	Ile	Thr	Ser	Ala	Gly	Val	Ser	Phe	Gln	Ser	Pro	Leu	Met	Ser	Leu
210					165					170					175	
211																
212	Gln	Pro	Met	Leu	Val	Val	Lys	Pro	Asp	Pro	Pro	Leu	Gly	Leu	His	Met
213				180					185					190		
214																
215	Glu	Val	Thr	Asp	Asp	Gly	Asn	Leu	Lys	Ile	Ser	Trp	Asp	Ser	Gln	Thr
216			195					200					205			
217																
218	Met	Ala	Pro	Phe	Pro	Leu	Gln	Tyr	Gln	Val	Lys	Tyr	Leu	Glu	Asn	Ser
219		210					215					220				
220																
221	Thr	Ile	Val	Arg	Glu	Ala	Ala	Glu	Ile	Val	Ser	Ala	Thr	Ser	Leu	Leu
222	225					230					235					240
223																
224	Val	Asp	Ser	Val	Leu	Pro	Gly	Ser	Ser	Tyr	Glu	Val	Gln	Val	Arg	Ser
225					245					250					255	
226																
227	Lys	Arg	Leu	Asp	Gly	Ser	Gly	Val	Trp	Ser	Asp	Trp	Ser	Ser	Pro	Gln
228			260						265					270		
229																
230	Val	Phe	Thr	Thr	Gln	Asp	Val	Val	Tyr	Phe	Pro	Pro	Lys	Ile	Leu	Thr
231			275					280					285			
232																
233	Ser	Val	Gly	Ser	Asn	Ala	Ser	Phe	His	Cys	Ile	Tyr	Lys	Asn	Glu	Asn
234		290					295					300				
235																
236	Gln	Ile	Ile	Ser	Ser	Lys	Gln	Ile	Val	Trp	Trp	Arg	Asn	Leu	Ala	Glu
237	305					310					315					320
238																
239	Lys	Ile	Pro	Glu	Ile	Gln	Tyr	Ser	Ile	Val	Ser	Asp	Arg	Val	Ser	Lys
240					325					330					335	
241																
242	Val	Thr	Phe	Ser	Asn	Leu	Lys	Ala	Thr	Arg	Pro	Arg	Gly	Lys	Phe	Thr
243				340					345					350		
244																
245	Tyr	Asp	Ala	Val	Tyr	Cys	Cys	Asn	Glu	Gln	Ala	Cys	His	His	Arg	Tyr
246			355					360					365			
247																
248	Ala	Glu	Leu	Tyr	Val	Ile	Asp	Val	Asn	Ile	Asn	Ile	Ser	Cys	Glu	Thr
249		370					375					380				
250																
251	Asp	Gly	Tyr	Leu	Thr	Lys	Met	Thr	Cys	Arg	Trp	Ser	Pro	Ser	Thr	Ile
252	385					390					395					400
253																
254	Gln	Ser	Leu	Val	Gly	Ser	Thr	Val	Gln	Leu	Arg	Tyr	His	Arg	Arg	Ser
255					405					410					415	
256																
257	Leu	Tyr	Cys	Pro	Asp	Ser	Pro	Ser	Ile	His	Pro	Thr	Ser	Glu	Pro	Lys
258				420					425					430		

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